

AMENDMENTS TO THE SPECIFICATION

Please amend the specification as indicated herein.

Please delete paragraph [0148] and replace it with the following rewritten paragraph:

[0148] A preferred detection method is allele specific hybridization using probes overlapping the polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the polymorphic region. Examples of probes for detecting specific allelic variants of the polymorphic region located in intron X are probes comprising a nucleotide sequence set forth in any of SEQ ID NO. X. In a preferred embodiment of the invention, several probes capable of hybridizing specifically to allelic variants are attached to a solid phase support, e.g., a "chip." Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up to 250,000 oligonucleotides (GeneChip, Affymetrix). Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al., HUMAN MUTATION 7:244 (1996) and in Kozal et al., NATURE MEDICINE 2:753 (1996). In one embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment. For example, the identity of the allelic variant of the nucleotide polymorphism of nucleotide A or G at position 33 of Seq ID-1 (baySNP179) and that of other possible polymorphic regions can be determined in a single hybridization experiment.

Please delete paragraph [0272] and replace it with the following rewritten paragraph:

TABLE 2a

OLIGONUCLEOTIDE PRIMERS USED FOR GENOTYPING USING MASS SPECTROMETRY

[0272] The baySNP number refers to an internal numbering of the PA SNPs. Primer sequences are listed for preamplification of the genomic fragments (primers EF and ER) and for subsequent allele specific PCR of the SNP.

baySNP	SNP	NAM E	SEQUENCE	<u>SEQ ID NO:</u>
160	C195T	ER	gacgatgccttcagcacaCTTGGCTTGAATAGAGA	<u>1</u>
160	C195T	EF	GACTATGCGGAGAAAGATG	<u>2</u>
160	C195T	CF	gggacggtcggtagatCTGAGCTGTGAGAGGGGC	<u>3</u>
160	C195T	TF	gctggctcggtcaagaCTGAGCTGTGAGAGGGGT	<u>4</u>
1278	A168G	AF	gggacggtcggtagatGCCGCCAGAGCAAGCTA	<u>5</u>
1278	A168G	EF	CACTACAGATAGAGGGGTG	<u>6</u>
1278	A168G	ER	GACGATGCCTTCAGCACAAATTGAGATGACAGGTTGAG	<u>7</u>
1278	A168G	GF	gctggctcggtcaagaGCCGCCAGAGCAAGCTG	<u>8</u>
1371	C507T	CR	gggacggtcggtagatGGCTCGGACGATGGGAG	<u>9</u>
1371	C507T	EF	GACGATGCCTTCAGCACAGCCCACTCCTACCACAAG	<u>10</u>
1371	C507T	ER	GGGGACAGAGAGAACCAA	<u>11</u>
1371	C507T	TR	gctggctcggtcaagaGGCTCGGACGATGGGAA	<u>12</u>
1806	A201G	AF	gggacggtcggtagatTGGCGTCCTGGTGGCA	<u>13</u>
1806	A201G	EF	TCTCGGGCTAACTCTT	<u>14</u>
1806	A201G	ER	GACGATGCCTTCAGCACACTGTCACTCCAAACCTTCT	<u>15</u>
1806	A201G	GF	gctggctcggtcaagaTGGCGTCCTGGTGGCG	<u>16</u>
2178	C719T	CR	gggacggtcggtagatTGGCAAACACGTTCCAGG	<u>17</u>
2178	C719T	EF	GACGATGCCTTCAGCACAAAGGAAATAGAAGGGAGGA	<u>18</u>
2178	C719T	ER	CCTGTGAAC TGCTGAAC	<u>19</u>
2178	C719T	TR	gctggctcggtcaagaTGGCAAACACGTTCCAGA	<u>20</u>
2198	C548T	CF	gggacggtcggtagatGACAAATGCTTATGAAAC	<u>21</u>
2198	C548T	EF	GAAATAACTAGGCGTGG	<u>22</u>
2198	C548T	ER	GACGATGCCTTCAGCACATGGGAAAAATAACAAAG	<u>23</u>
2198	C548T	TF	gctggctcggtcaagaGACAAATGCTTATGAAAT	<u>24</u>
2214	A231T	AR	gggacggtcggtagatTTGGCTGCACTGCGAAGT	<u>25</u>
2214	A231T	EF	GACGATGCCTTCAGCACAGGAAGGTGAAGGAGAGA	<u>26</u>
2214	A231T	ER	GTAGGCATTGTTGGTATG	<u>27</u>
2214	A231T	TR	gctggctcggtcaagaTTGGCTGCACTGCGAAGA	<u>28</u>
2267	C490T	CR	gggacggtcggtagatATTCTGGCACCACAGCCG	<u>29</u>

baySNP	SNP	NAM E	SEQUENCE	<u>SEQ ID NO:</u>
2267	C490T	EF	GACGATGCCTTCAGCACACTTCTGAGTGGCGTTATTAC	<u>30</u>
2267	C490T	ER	GGTGGCCAAGGTCGTGCTG	<u>31</u>
2267	C490T	TR	gctggctcggtcaagaATTCTGGGCACCACAGCCA	<u>32</u>
3907	A194C	ER	gacgatgccttcagcacaAGTGGAGAGAGGATGTTAG	<u>33</u>
3907	A194C	EF	GTCTTATGTAGACGCTTGG	<u>34</u>
3907	A194C	AF	gggacggtcggtagatTCCCCAGGGCGGGTAAGA	<u>35</u>
3907	A194C	CF	gctggctcggtcaagaTCCCCAGGGCGGGTAAGC	<u>36</u>
4564	A446G	EF	gacgatgccttcagcacaAACTCTGCTCCATATTCC	<u>37</u>
4564	A446G	ER	CTCCATCATCCTTTACAC	<u>38</u>
4564	A446G	AR	gggacggtcggtagatACGGCTCCTATTCCCAGT	<u>39</u>
4564	A446G	GR	gctggctcggtcaagaACGGCTCCTATTCCCAGC	<u>40</u>
5569	A605G	ER	gacgatgccttcagcacaCCTCTGTTCCCTCCCTCT	<u>41</u>
5569	A605G	EF	AGTGTGGTCTCCGAATGT	<u>42</u>
5569	A605G	AF	gggacggtcggtagatTGGAGCATGGGAGGCCACA	<u>43</u>
5569	A605G	GF	gctggctcggtcaagaTGGAGCATGGGAGGCCACG	<u>44</u>
6872	A254G	EF	CATCAAGGCAGACCAA	<u>45</u>
6872	A254G	ER	GAAGGAGAGCAAAGGG	<u>46</u>
6872	A254G	AF	gggacggtcggtagatAAGATACCTAAATAACAA	<u>47</u>
6872	A254G	GF	gctggctcggtcaagaAAGATACCTAAATAACAG	<u>48</u>
8164	A251T	EF	CACAAAATACACCAACAA	<u>49</u>
8164	A251T	ER	CATTGATAAGGAATAAGGA	<u>50</u>
8164	A251T	AF	gggacggtcggtagatACATACGCACAAAAATTAA	<u>51</u>
8164	A251T	TF	gctggctcggtcaagaACATACGCACAAAAATT	<u>52</u>
8242	A251G	EF	AGACCCACATTCACACAC	<u>53</u>
8242	A251G	ER	TTACACGTCAAGCTTCCTC	<u>54</u>
8242	A251G	AR	gggacggtcggtagatTTACACACACAGTTAGAT	<u>55</u>
8242	A251G	GR	gctggctcggtcaagaTTACACACACAGTTAGAC	<u>56</u>
8589	C378T	EF	gacgatgccttcagcacaGTTGTTGGTTGTTGTTT	<u>57</u>
8589	C378T	ER	GCTTGGCTTCCTATGTCT	<u>58</u>
8589	C378T	CR	gggacggtcggtagatTAGCATCAATGCTGGGAG	<u>59</u>
8589	C378T	TR	gctggctcggtcaagaTAGCATCAATGCTGGGAA	<u>60</u>
10771	C64G	EF	gacgatgccttcagcacaCCAGGGAAAGAGCAGAAC	<u>61</u>
10771	C64G	ER	TGTACGGGAAGAGGCAGA	<u>62</u>
10771	C64G	CR	gggacggtcggtagatAGGGTGACACAGGCCACG	<u>63</u>
10771	C64G	GR	gctggctcggtcaagaAGGGTGACACAGGCCACC	<u>64</u>
12399	A55G	EF	gacgatgccttcagcacaGTGTGTTCGCAGGAGGA	<u>65</u>
12399	A55G	ER	AGTTCTCTGGCTGGTGTG	<u>66</u>

baySNP	SNP	NAME	SEQUENCE	<u>SEQ ID NO:</u>
12399	A55G	AR	gggacggtcggtagatTAGGGGGCTGCCAGGCTT	<u>67</u>
12399	A55G	GR	gctggctcggtcaagaTAGGGGGCTGCCAGGCTC	<u>68</u>

Please delete paragraph [0273] and replace it with the following rewritten paragraph:

TABLE 2b

OLIGONUCLEOTIDE PRIMERS USED FOR GENOTYPING USING PYROSEQUENCING

[0273] The baySNP number refers to an internal numbering of the PA SNPs. Primer sequences are listed for preamplification of the genomic fragments and for sequencing of the SNP using the pyrosequencing method. Bio: Biotinylated Oligonucleotide.

baySNP	NAME	SEQUENCE	<u>SEQ ID NO:</u>
7372	Primer F	GTGGAGCGGGAGCGAAC	<u>69</u>
7372	Primer R	Bio-CCCCTCAAACCGTCAG	<u>70</u>
7372	Seq.	GGGCATTCTCAGTGG	<u>71</u>
900066	Primer F	BIO-TGCCGGGAACGTGGACTAGA	<u>72</u>
900066	Primer R	CCGGCCTCTGTTATGTAGTTCA	<u>73</u>
900066	Seq.	CTTCCCCGGCCGGGCCGCC	<u>74</u>
900073	Primer F	BIO-GGCCCGGCTCCACGTGCTTC	<u>75</u>
900073	Primer R	TGAGAACCGGCTCTGTTGGTGC	<u>76</u>
900073	Seq.	CTGTGCTCTCCCTCCCTCCCC	<u>77</u>

Please delete paragraph [0274], including the heading, and replace it with the following rewritten paragraph:

TABLE 2d TABLE 2c

OLIGONUCLEOTIDE PRIMERS USED FOR GENOTYPING USING TAQMAN

[0274] The baySNP number refers to an internal numbering of the PA SNPs. Primer sequences are listed for amplification of the genomic fragments. In addition the respective fluorescent hybridisation probes are listed. If not otherwise stated, all fluorescent probes have a 'minor groove binder' (MGB) attached (Kutyavin et al., Nucleic Acids Research 2000, NUCLEIC ACIDS RESEARCH 28:655-661 (2000)).

baySNP	F-SEQUENCE	R-SEQUENCE	VIC-MGB	FAM-MGB
1278	ACCGAGCTGGAGGGGAGTT <u>(SEQ ID NO: 78)</u>	CACAGCCTGGCCACCTAAC <u>(SEQ ID NO: 80)</u>	CAGAGCAAGCTaAGGA <u>(SEQ ID NO: 82)</u>	AGAGCAAGCTgAGGAG <u>(SEQ ID NO: 84)</u>
10771	CTGGGCCACCGAGTTAC <u>(SEQ ID NO: 79)</u>	GATCTCTGTGAGTGTGCGTCTGT <u>(SEQ ID NO: 81)</u>	AGGAAGGcGTGGCCT <u>(SEQ ID NO: 83)</u>	CAAGGAAGGgGTGGC <u>(SEQ ID NO: 85)</u>